

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2003, 13:48:12 ; Search time 0.001 Seconds

(without alignments)
178.084 Million cell updates/sec

Title: us-09-869-540a-11

Perfect score: 2212
Sequence: 1 MSVGAMKKGVGRAVGLGGSS.....LRAVSNQTADEERTESKGT 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 422 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : us-09-478-601-2.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	2207	99.8	422	1	us-09-478-601-2

ALIGNMENTS

RESULT 1
us-09-478-601-2

Query Match 99.8% ; Score 2207 ; DB 1 ; Length 422 ;
Best Local Similarity 99.8% ; Pred. No. 0 ;
Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSVGAMKKGVGRAVGLGGSSCCATDEEDPLPNCGACAPGGGRRRLPPPAWEGSSARL 60
DB	1	MSVGAMKKGVGRAVGLGGSSCCATDEEDPLPDCGACAPGGGRRRLPPPAWEGSSARL 60
QY	61	WEQATGTGMDLEASLPTGPNASNTSDGPDNLTSAGSPRTGISYINIMPSVGTIC 120
DB	61	WEQATGTGMDLEASLPTGPNASNTSDGPDNLTSAGSPRTGISYINIMPSVGTIC 120
QY	121	LLGIGNSTYIFAVVKKSKLHMCNNVPDIFIINLSVVDLLFLGMPFIHQLMGNCVHF 180
DB	121	LLGIGNSTYIFAVVKKSKLHMCNNVPDIFIINLSVVDLLFLGMPFIHQLMGNCVHF 180
QY	181	GETMCTLTAMDANSOFTSTYIILTAMADRYLATVHPISSTKRKPSVATLYCLMAL 240
DB	181	GETMCTLTAMDANSOFTSTYIILTAMADRYLATVHPISSTKRKPSVATLYCLMAL 240
QY	241	FISITPYMLYARLIPPGAVGCGIRLPNDTDLVFTLYOFLAFALPFWVITAAVRI 300
DB	241	FISITPYMLYARLIPPGAVGCGIRLPNDTDLVFTLYOFLAFALPFWVITAAVRI 300

QY	301	LQRTSSVAPASORSIRLRTKRYRTAATCIQVFVGCWAPYVLTQLTQLSISRPTLFVY 360
DB	301	LQRTSSVAPASORSIRLRTKRYRTAATCIQVFVGCWAPYVLTQLTQLSISRPTLFVY 360
QY	361	LYNNAISLGYANSCLNPFYIIVLCETFERKRLVSVKPAAGOLRAVSNQTADEERTESK 420
DB	361	LYNNAISLGYANSCLNPFYIIVLCETFERKRLVSVKPAAGOLRAVSNQTADEERTESK 420
QY	421	GT 422
DB	421	GT 422

Search completed: July 7, 2003, 13:48:13
Job time : 1 secs

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OM protein - protein search, using sw model

Run on: July 7, 2003, 13:42:55 ; Search time 0.001 Seconds
(without alignments)
148.966 Million cell updates/sec

Title: us-09-869-540a-11

Perfect score: 2212
Sequence: 1 MSVGAMKMGKGVRAVLGGGS.....LRAVSNQADERTESKGT 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 353 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : us-09-925-776-2 *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1824	82.5	353	1	us-09-925-776-2

ALIGNMENTS

RESULT 1
us-09-925-776-2

Query Match 82.5% ; Score 1824 ; DB 1 ; Length 353 ;
Best Local Similarity 100.0% ; Pred. No. 0 ;
Matches 353 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

QY	70	MDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIIIMPVFGTICLIGTIGNST	129
DB	1	MDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIIIMPVFGTICLIGTIGNST	60
QY	130	VIFAVVYKSKLHMCNNPDIIFIINLSYVDLFLGMPMTIHLGNGVWHFGETMCTLT	189
DB	61	VIFAVVYKSKLHMCNNPDIIFIINLSYVDLFLGMPMTIHLGNGVWHFGETMCTLT	120
QY	190	AMDANSQFTSTYILTATAIDRYLATVHPISSTKFRKPSVATLYICLLMALSFISTIPVWL	249
DB	121	AMDANSQFTSTYILTATAIDRYLATVHPISSTKFRKPSVATLYICLLMALSFISTIPVWL	180
QY	250	YARLIPEPGGAVCGGIRLPNDTLYWFTLYQFLAFALPFVYITAAVYRIIQRMTSSVA	309
DB	181	YARLIPEPGGAVCGGIRLPNDTLYWFTLYQFLAFALPFVYITAAVYRIIQRMTSSVA	240
QY	310	PASORSIRLRTKRVTAICLVFVCNAPYVVLQTLQSLSTSPFLTFVYLYMAISLG	369
DB	241	PASORSIRLRTKRVTAICLVFVCNAPYVVLQTLQSLSTSPFLTFVYLYMAISLG	300

QY 370 YANSCINPEYIYIVLCETFRKRLVSVKPAAGOLRAVSNQADERTESKGT 422
DB 301 YANSCINPEYIYIVLCETFRKRLVSVKPAAGOLRAVSNQADERTESKGT 353

Search completed: July 7, 2003, 13:42:55
Job time : 0.001 secs